## Pathways Enriched for Genes Significantly Expressed in Response to Arsenic

Category	Differentially Expressed	Size	P value	Significant
KEGG PATHWAY	Differentially Expressed	0120	i value	Olgimicant
Cell Cycle Reference Pathway	•	87	0.9072	FALSE
Galcatose Metabolism	8 5	67 15	0.9072	FALSE
Glutathione Metabolism	6	11	0.0391	TRUE
	7	55	0.609	FALSE
MAPK Signalling Pathway  Methionine Metabolism	8	11	1.07E-05	TRUE
Proteasome	9	30	0.0127	FALSE
Purine Metabolism	14	139	0.8991	FALSE
Pyrmidine metabolism	8	80	0.8515	FALSE
Sulfur Metabolism	7	7	7.15E-07	TRUE
Serine, Threonine and Glycine Metabolism	8	25	0.0125	FALSE
Citrate Cycle	4	22	0.3345	FALSE
Starch and Sucrose	9	31	0.0159	FALSE
Pyruvate	4	25	0.4292	FALSE
Reductive Carboxylate	5	16	0.0508	FALSE
Second Messenger Signaling	3	19	0.472	FALSE
Valine, Leucine, Isoleucine	2	13	0.5313	FALSE
Circadian rhythm	2	19	0.7398	FALSE
Porphyrin and chlorophyll metabolism	- 7	74	0.8782	FALSE
Selenoamino acid metabolism	10	12	8.36E-08	TRUE
Ubiquitin mediated proteolysis	2	29	0.9133	FALSE
Cysteine Metabolism	2	4	0.088	FALSE
Fructose and Mannose	6	15	0.0093	FALSE
Carbon Fixation	3	15	0.3207	FALSE
Alanine and Aspartate	2	24	0.8477	FALSE
Glutamate	3	19	0.472	FALSE
Methane	2	4	0.088	FALSE
SIMPLIFIED ONTOLOGY (Biological Process)				
Biological Process	72	436	0.0244	FALSE
Cell Communcation	72	270	<1.00E-008	TRUE
Cell Growth and Maintenance	47	268	0.0231	FALSE
Cell Surface Linked Signal Transduction	14	91	0.3197	FALSE
Developmental Processes	5	32	0.4233	FALSE
Heat Shock response	14	22	5.40E-08	TRUE
Intracelluar Signalling	9	47	0.1635	FALSE
Serine Threonine kinase Signalling	5	38	0.5815	FALSE
Signal Transduction	26	172	0.2656	FALSE
ATPase	3	78	0.9988	FALSE
Cyclin	4	29	0.5499	FALSE

Table 1. Transcript profiling reveals arsenic affects glutathione, methionine, sulfur, selenoaminoacid metabolism, cell communication and heat shock response. Genes were categorized by Kegg pathway and Simplified Gene Ontology. In total, 894 genes out of 6240 had a significant alteration in expression. Along with the size of each functional category, a statistical measure for the significance of the enrichment was calculated by using a hypergeometric test. The level of significance for this test (i.e. True, False) was determined using the Bonferroni correction, where the  $\alpha$  value is set at 0.05 and 27 and 11 tests were done for Kegg pathway and Simplified Ontology, respectively.